



RAW SEQUENCE LISTING ERROR REPORT

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Application Serial Number: 10/613,053
Source: OIPE
Date Processed by STIC: 7/29/2003

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- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

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VERSION 4.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
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1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)

2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450

3. Hand Carry directly to:

U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202

Or

U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 04/24/2003



OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/613,053

DATE: 07/29/2003

TIME: 11:29:14

Input Set : A:\PTO.YF.txt

Output Set: N:\CRF4\07292003\J613053.raw

2 <110> APPLICANT: Mitsubishi Chemical Corporation
 W--> 3 <120> TITLE OF INVENTION: A protein which is involved in recovery of cytoplasm male fertility from
 W--> 4 sterility and a gene encoding the protein
 W--> 5 <130> FILE REFERENCE: A21220A
 C--> 6 <140> CURRENT APPLICATION NUMBER: US/10/613,053
 C--> 6 <141> CURRENT FILING DATE: 2003-07-07
 E--> 6 <160> NUMBER OF SEQ ID: 39

41 (p. 15)

pp 1, 4-5, 8, 10-15

ERRORED SEQUENCES

531 <210> SEQ ID NO: 16

532 <211> LENGTH: 2064

533 <212> TYPE: DNA

534 <213> ORGANISM: Raphanus sativus

OK--> 535 <400> SEQUENCE: 16

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537 Met Leu Ala Arg Val Cys Gly Phe Lys Cys Ser Ser Ser Pro Ala Glu

538 1 5 10 15

539 tct gcg gct aga ttg ttc tgt acg aga tcg att cgt gat act ctg gcc 96

540 Ser Ala Ala Arg Leu Phe Cys Thr Arg Ser Ile Arg Asp Thr Leu Ala

541 20 25 30

542 aag gca agc gga gag agt tgc gaa gca ggt ttt gga gga gag agt ttg 144

543 Lys Ala Ser Gly Glu Ser Cys Glu Ala Gly Phe Gly Gly Glu Ser Leu

544 35 40 45

545 aag ctg caa agt ggg ttt cat gaa atc aaa ggt tta gag gat gcg att 192

546 Lys Leu Gln Ser Gly Phe His Glu Ile Lys Gly Leu Glu Asp Ala Ile

547 50 55 60

548 gat ttg ttc agt gac atg ctt cga tct cgt cct tta cct tct gtg gtt 240

549 Asp Leu Phe Ser Asp Met Leu Arg Ser Arg Pro Leu Pro Ser Val Val

550 65 70 75 80

551 gat ttc tgt aaa ttg atg ggt gtg gtg gtg aga atg gaa cgc ccg gat 288

552 Asp Phe Cys Lys Leu Met Gly Val Val Val Arg Met Glu Arg Pro Asp

553 85 90 95

554 ctt gtg att tct ctc tat cag aag atg gaa agg aaa cag att cga tgt 336

555 Leu Val Ile Ser Leu Tyr Gln Lys Met Glu Arg Lys Gln Ile Arg Cys

556 100 105 110

557 gat ata tac agc ttc aat att ctg ata aaa tgt ttc tgc agc tgc tct 384

558 Asp Ile Tyr Ser Phe Asn Ile Leu Ile Lys Cys Phe Cys Ser Cys Ser

559 115 120 125

560 aag ctc ccc ttt gct ttg tct aca ttt ggt aag ctc acc aag ctt gga 432

561 Lys Leu Pro Phe Ala Leu Ser Thr Phe Gly Lys Leu Thr Lys Leu Gly

562 130 135 140

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563 ctc cac cct gat gtt gtt acc ttc acc acc ctg ctc cac gga ttg tgc 480
564 Leu His Pro Asp Val Val Thr Phe Thr Thr Leu Leu His Gly Leu Cys
565 145 150 155 160
566 gtg gaa gat agg gtt tct gaa gct ttg aat ttg ttt cat caa atg ttt 528
567 Val Glu Asp Arg Val Ser Glu Ala Leu Asn Leu Phe His Gln Met Phe
568 165 170 175
569 gaa acg aca tgt agg ccc aat gtc gta acc ttc acc act ttg atg aac 576
570 Glu Thr Thr Cys Arg Pro Asn Val Val Thr Phe Thr Thr Leu Met Asn
571 180 185 190
572 ggt ctt tgc cgc gag ggt aga att gtc gaa gcc gta gct ctg ctt gat 624
573 Gly Leu Cys Arg Glu Gly Arg Ile Val Glu Ala Val Ala Leu Leu Asp
574 195 200 205
575 cgg atg atg gaa gat ggt ctc cag cct acc cag att act tat gga aca 672
576 Arg Met Met Glu Asp Gly Leu Gln Pro Thr Gln Ile Thr Tyr Gly Thr
577 210 215 220
578 atc gta gat ggg atg tgt aag aag gga gat act gtg tct gca ctg aat 720
579 Ile Val Asp Gly Met Cys Lys Lys Gly Asp Thr Val Ser Ala Leu Asn
580 225 230 235 240
581 ctg ctg agg aag atg gag gag gtg agc cac atc ata ccc aat gtt gta 768
582 Leu Leu Arg Lys Met Glu Glu Val Ser His Ile Ile Pro Asn Val Val
583 245 250 255
584 atc tat agt gca atc att gat agc ctt tgt aaa gac gga cgt cat agc 816
585 Ile Tyr Ser Ala Ile Ile Asp Ser Leu Cys Lys Asp Gly Arg His Ser
586 260 265 270
587 gat gca caa aat ctt ttc act gaa atg caa gag aaa gga atc ttt ccc 864
588 Asp Ala Gln Asn Leu Phe Thr Glu Met Gln Glu Lys Gly Ile Phe Pro
589 275 280 285
590 gat tta ttt acc tac aac agt atg ata gtt ggt ttt tgt agc tct ggt 912
591 Asp Leu Phe Thr Tyr Asn Ser Met Ile Val Gly Phe Cys Ser Ser Gly
592 290 295 300
593 aga tgg agc gac gcg gag cag ttg ttg caa gaa atg tta gaa agg aag 960
594 Arg Trp Ser Asp Ala Glu Gln Leu Leu Gln Glu Met Leu Glu Arg Lys
595 305 310 315 320
596 atc agc cct gat gtt gta act tat aat gct ttg atc aat gca ttt gtc 1008
597 Ile Ser Pro Asp Val Val Thr Tyr Asn Ala Leu Ile Asn Ala Phe Val
598 325 330 335
599 aag gaa ggc aag ttc ttt gag gct gaa gaa tta tac gat gag atg ctt 1056
600 Lys Glu Gly Lys Phe Phe Glu Ala Glu Glu Leu Tyr Asp Glu Met Leu
601 340 345 350
602 cca agg ggt ata atc cct aat aca atc aca tat agt tca atg atc gat 1104
603 Pro Arg Gly Ile Ile Pro Asn Thr Ile Thr Tyr Ser Ser Met Ile Asp
604 355 360 365
605 gga ttt tgc aaa cag aat cgt ctt gat gct gct gag cac atg ttt tat 1152
606 Gly Phe Cys Lys Gln Asn Arg Leu Asp Ala Ala Glu His Met Phe Tyr
607 370 375 380
608 ttg atg gct acc aag ggc tgc tct ccc aac cta atc act ttc aat act 1200
609 Leu Met Ala Thr Lys Gly Cys Ser Pro Asn Leu Ile Thr Phe Asn Thr
610 385 390 395 400
611 ctc ata gac gga tat tgt ggg gct aag agg ata gat gat gga atg gaa 1248

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612 Leu Ile Asp Gly Tyr Cys Gly Ala Lys Arg Ile Asp Asp Gly Met Glu
613          405          410          415
614 ctt ctc cat gag atg act gaa aca gga tta gtt gct gac aca act act 1296
615 Leu Leu His Glu Met Thr Glu Thr Gly Leu Val Ala Asp Thr Thr Thr
616          420          425          430
617 tac aac act ctt att cac ggg ttc tat ctg gtg ggc gat ctt aat gct 1344
618 Tyr Asn Thr Leu Ile His Gly Phe Tyr Leu Val Gly Asp Leu Asn Ala
619          435          440          445
620 gct cta gac ctt tta caa gag atg atc tct agt ggt ttg tgc cct gat 1392
621 Ala Leu Asp Leu Leu Gln Glu Met Ile Ser Ser Gly Leu Cys Pro Asp
622          450          455          460
623 atc gtt act tgt gac act ttg ctg gat ggt ctc tgc gat aat ggg aaa 1440
624 Ile Val Thr Cys Asp Thr Leu Leu Asp Gly Leu Cys Asp Asn Gly Lys
625 465          470          475          480
626 cta aaa gat gca ttg gaa atg ttt aag gtt atg cag aag agt aag aag 1488
627 Leu Lys Asp Ala Leu Glu Met Phe Lys Val Met Gln Lys Ser Lys Lys
628          485          490          495
629 gat ctt gat gct agt cac ccc ttc aat ggt gtg gaa cct gat gtt caa 1536
630 Asp Leu Asp Ala Ser His Pro Phe Asn Gly Val Glu Pro Asp Val Gln
631          500          505          510
632 act tac aat ata ttg atc agc ggc ttg atc aat gaa ggg aag ttt tta 1584
633 Thr Tyr Asn Ile Leu Ile Ser Gly Leu Ile Asn Glu Gly Lys Phe Leu
634          515          520          525
635 gag gcc gag gaa tta tac gag gag atg ccc cac agg ggt ata gtc cca 1632
636 Glu Ala Glu Glu Leu Tyr Glu Glu Met Pro His Arg Gly Ile Val Pro
637          530          535          540
638 gat act atc acc tat agc tca atg atc gat gga tta tgc aag cag agc 1680
639 Asp Thr Ile Thr Tyr Ser Ser Met Ile Asp Gly Leu Cys Lys Gln Ser
640 545          550          555          560
641 cgc cta gat gag gct aca caa atg ttt gat tcg atg ggt agc aag agc 1728
642 Arg Leu Asp Glu Ala Thr Gln Met Phe Asp Ser Met Gly Ser Lys Ser
643          565          570          575
644 ttc tct cca aac gta gtg acc ttt act aca ctc att aat ggc tac tgt 1776
645 Phe Ser Pro Asn Val Val Thr Phe Thr Thr Leu Ile Asn Gly Tyr Cys
646          580          585          590
647 aag gca gga agg gtt gat gat ggg ctg gag ctt ttc tgc gag atg ggt 1824
648 Lys Ala Gly Arg Val Asp Asp Gly Leu Glu Leu Phe Cys Glu Met Gly
649          595          600          605
650 cga aga ggg ata gtt gct aac gca att act tac atc act ttg att tgt 1872
651 Arg Arg Gly Ile Val Ala Asn Ala Ile Thr Tyr Ile Thr Leu Ile Cys
652          610          615          620
653 ggt ttt cgt aaa gtg ggt aat att aat ggg gct cta gac att ttc cag 1920
654 Gly Phe Arg Lys Val Gly Asn Ile Asn Gly Ala Leu Asp Ile Phe Gln
655 625          630          635          640
656 gag atg att tca agt ggt gtg tat cct gat acc att acc atc cgc aat 1968
657 Glu Met Ile Ser Ser Gly Val Tyr Pro Asp Thr Ile Thr Ile Arg Asn
658          645          650          655
659 atg ctg act ggt tta tgg agt aaa gag gaa cta aaa agg gca gtg gca 2016
660 Met Leu Thr Gly Leu Trp Ser Lys Glu Glu Leu Lys Arg Ala Val Ala

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661
 662 atg ctt gag aaa ctg cag atg agt atg gat cta tca ttt ggg gga tga 2064
 E--> 663 Met Leu Glu Lys Leu Gln Met Ser Met Asp Leu Ser Phe Gly Gly Xaa
 664 675 680 685
 665 <210> SEQ ID NO: 17
 666 <211> LENGTH: 688
 667 <212> TYPE: PRT
 668 <213> ORGANISM: Raphanus sativus
 @6-> 669 <400> SEQUENCE: 17
 670 Met Leu Ala Arg Val Cys Gly Phe Lys Cys Ser Ser Ser Pro Ala Glu
 671 1 5 10 15
 672 Ser Ala Ala Arg Leu Phe Cys Thr Arg Ser Ile Arg Asp Thr Leu Ala
 673 20 25 30
 674 Lys Ala Ser Gly Glu Ser Cys Glu Ala Gly Phe Gly Gly Glu Ser Leu
 675 35 40 45
 676 Lys Leu Gln Ser Gly Phe His Glu Ile Lys Gly Leu Glu Asp Ala Ile
 677 50 55 60
 678 Asp Leu Phe Ser Asp Met Leu Arg Ser Arg Pro Leu Pro Ser Val Val
 679 65 70 75 80
 680 Asp Phe Cys Lys Leu Met Gly Val Val Val Arg Met Glu Arg Pro Asp
 681 85 90 95
 682 Leu Val Ile Ser Leu Tyr Gln Lys Met Glu Arg Lys Gln Ile Arg Cys
 683 100 105 110
 684 Asp Ile Tyr Ser Phe Asn Ile Leu Ile Lys Cys Phe Cys Ser Cys Ser
 685 115 120 125
 686 Lys Leu Pro Phe Ala Leu Ser Thr Phe Gly Lys Leu Thr Lys Leu Gly
 687 130 135 140
 688 Leu His Pro Asp Val Val Thr Phe Thr Thr Leu Leu His Gly Leu Cys
 689 145 150 155 160
 690 Val Glu Asp Arg Val Ser Glu Ala Leu Asn Leu Phe His Gln Met Phe
 691 165 170 175
 692 Glu Thr Thr Cys Arg Pro Asn Val Val Thr Phe Thr Thr Leu Met Asn
 693 180 185 190
 694 Gly Leu Cys Arg Glu Gly Arg Ile Val Glu Ala Val Ala Leu Leu Asp
 695 195 200 205
 696 Arg Met Met Glu Asp Gly Leu Gln Pro Thr Gln Ile Thr Tyr Gly Thr
 697 210 215 220
 698 Ile Val Asp Gly Met Cys Lys Lys Gly Asp Thr Val Ser Ala Leu Asn
 699 225 230 235 240
 700 Leu Leu Arg Lys Met Glu Glu Val Ser His Ile Ile Pro Asn Val Val
 701 245 250 255
 702 Ile Tyr Ser Ala Ile Ile Asp Ser Leu Cys Lys Asp Gly Arg His Ser
 703 260 265 270
 704 Asp Ala Gln Asn Leu Phe Thr Glu Met Gln Glu Lys Gly Ile Phe Pro
 705 275 280 285
 706 Asp Leu Phe Thr Tyr Asn Ser Met Ile Val Gly Phe Cys Ser Ser Gly
 707 290 295 300
 708 Arg Trp Ser Asp Ala Glu Gln Leu Leu Gln Glu Met Leu Glu Arg Lys
 709 305 310 315 320

delete Xaa
 Xaa can only represent a single amino acid, not a stop codon

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710 Ile Ser Pro Asp Val Val Thr Tyr Asn Ala Leu Ile Asn Ala Phe Val
711           325           330           335
712 Lys Glu Gly Lys Phe Phe Glu Ala Glu Glu Leu Tyr Asp Glu Met Leu
713           340           345           350
714 Pro Arg Gly Ile Ile Pro Asn Thr Ile Thr Tyr Ser Ser Met Ile Asp
715           355           360           365
716 Gly Phe Cys Lys Gln Asn Arg Leu Asp Ala Ala Glu His Met Phe Tyr
717           370           375           380
718 Leu Met Ala Thr Lys Gly Cys Ser Pro Asn Leu Ile Thr Phe Asn Thr
719 385           390           395           400
720 Leu Ile Asp Gly Tyr Cys Gly Ala Lys Arg Ile Asp Asp Gly Met Glu
721           405           410           415
722 Leu Leu His Glu Met Thr Glu Thr Gly Leu Val Ala Asp Thr Thr Thr
723           420           425           430
724 Tyr Asn Thr Leu Ile His Gly Phe Tyr Leu Val Gly Asp Leu Asn Ala
725           435           440           445
726 Ala Leu Asp Leu Leu Gln Glu Met Ile Ser Ser Gly Leu Cys Pro Asp
727           450           455           460
728 Ile Val Thr Cys Asp Thr Leu Leu Asp Gly Leu Cys Asp Asn Gly Lys
729 465           470           475           480
730 Leu Lys Asp Ala Leu Glu Met Phe Lys Val Met Gln Lys Ser Lys Lys
731           485           490           495
732 Asp Leu Asp Ala Ser His Pro Phe Asn Gly Val Glu Pro Asp Val Gln
733           500           505           510
734 Thr Tyr Asn Ile Leu Ile Ser Gly Leu Ile Asn Glu Gly Lys Phe Leu
735           515           520           525
736 Glu Ala Glu Glu Leu Tyr Glu Glu Met Pro His Arg Gly Ile Val Pro
737           530           535           540
738 Asp Thr Ile Thr Tyr Ser Ser Met Ile Asp Gly Leu Cys Lys Gln Ser
739 545           550           555           560
740 Arg Leu Asp Glu Ala Thr Gln Met Phe Asp Ser Met Gly Ser Lys Ser
741           565           570           575
742 Phe Ser Pro Asn Val Val Thr Phe Thr Thr Leu Ile Asn Gly Tyr Cys
743           580           585           590
744 Lys Ala Gly Arg Val Asp Asp Gly Leu Glu Leu Phe Cys Glu Met Gly
745           595           600           605
746 Arg Arg Gly Ile Val Ala Asn Ala Ile Thr Tyr Ile Thr Leu Ile Cys
747           610           615           620
748 Gly Phe Arg Lys Val Gly Asn Ile Asn Gly Ala Leu Asp Ile Phe Gln
749 625           630           635           640
750 Glu Met Ile Ser Ser Gly Val Tyr Pro Asp Thr Ile Thr Ile Arg Asn
751           645           650           655
752 Met Leu Thr Gly Leu Trp Ser Lys Glu Glu Leu Lys Arg Ala Val Ala
753           660           665           670
E--> 754 Met Leu Glu Lys Leu Gln Met Ser Met Asp Leu Ser Phe Gly Gly Xaa
755           675           680           685
756 <210> SEQ ID NO: 18
757 <211> LENGTH: 2073
758 <212> TYPE: DNA

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p.8

delete - Xaa
cannot
represent a
stop codon

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759 <213> ORGANISM: Raphanus sativus

W--> 760 <400> SEQUENCE: 18

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762 Met Leu Ala Arg Val Cys Gly Phe Lys Cys Ser Ser Ser Pro Ala Val
763 1 5 10 15
764 tct gcg gct aga ttg ttc tgt acg aga tcg att cgt gat act ctg gcc 96
765 Ser Ala Ala Arg Leu Phe Cys Thr Arg Ser Ile Arg Asp Thr Leu Ala
766 20 25 30
767 aag gca agc agg gat gga gag agt tgc gaa gca ggt ttt gga gga gag 144
768 Lys Ala Ser Arg Asp Gly Glu Ser Cys Glu Ala Gly Phe Gly Gly Glu
769 35 40 45
770 agt ttg aag ctg caa agt ggg ttt cat gaa atc aaa ggt tta gag gat 192
771 Ser Leu Lys Leu Gln Ser Gly Phe His Glu Ile Lys Gly Leu Glu Asp
772 50 55 60
773 gcg att gat ttg ttc agt gac atg ctt cga tct cgt cct tta cct tct 240
774 Ala Ile Asp Leu Phe Ser Asp Met Leu Arg Ser Arg Pro Leu Pro Ser
775 65 70 75 80
776 gtg gtt gat ttc tgt aaa ttg atg ggt gtg gtg gtg agg atg aaa cgc 288
777 Val Val Asp Phe Cys Lys Leu Met Gly Val Val Val Arg Met Lys Arg
778 85 90 95
779 ccg gat gtt gtg att tct ctc cat aag aag atg gaa atg cgg cgc att 336
780 Pro Asp Val Val Ile Ser Leu His Lys Lys Met Glu Met Arg Arg Ile
781 100 105 110
782 cca tgt gat gca tac agc ttc aat att ctg ata aag tgt ttc tgc agc 384
783 Pro Cys Asp Ala Tyr Ser Phe Asn Ile Leu Ile Lys Cys Phe Cys Ser
784 115 120 125
785 tgc tct aag ctg ccc ttt gct ttg tct aca ttt ggt aag ctc acc aag 432
786 Cys Ser Lys Leu Pro Phe Ala Leu Ser Thr Phe Gly Lys Leu Thr Lys
787 130 135 140
788 ctt gga ctc cac cct gat gtt gtt acc ttc acc acc ctt ctc cac gga 480
789 Leu Gly Leu His Pro Asp Val Val Thr Phe Thr Thr Leu Leu His Gly
790 145 150 155 160
791 ttg tgt gtg gaa aat agg ggt tct gaa gct ttg aat ttg ttt cat caa 528
792 Leu Cys Val Glu Asn Arg Gly Ser Glu Ala Leu Asn Leu Phe His Gln
793 165 170 175
794 atg ttt gaa acg rca tgt agg ccc aat gtc gta acc ttc acc act ttg 576
795 Met Phe Glu Thr Thr Cys Arg Pro Asn Val Val Thr Phe Thr Thr Leu
796 180 185 190
797 atg aac ggt ctt tgc cgc gag ggt aga att gtc gaa gcc gta gct cta 624
798 Met Asn Gly Leu Cys Arg Glu Gly Arg Ile Val Glu Ala Val Ala Leu
799 195 200 205
800 ctt gat cgg atg atg gaa gat ggt ctc cag cct acc cag att act tat 672
801 Leu Asp Arg Met Met Glu Asp Gly Leu Gln Pro Thr Gln Ile Thr Tyr
802 210 215 220
803 gga aca atc gta gat ggg atg tgt aag aag gga gat act gtg tct gca 720
804 Gly Thr Ile Val Asp Gly Met Cys Lys Lys Gly Asp Thr Val Ser Ala
805 225 230 235 240
806 ctg aat ctg ctg agg aag atg gag gag gtg agc cac atc ata ccc aat 768
807 Leu Asn Leu Leu Arg Lys Met Glu Glu Val Ser His Ile Ile Pro Asn

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808                               245                               250                               255
809 gtt gta atc tat agt gca atc att gat agc ctt tgt aaa gac gga cgt 816
810 Val Val Ile Tyr Ser Ala Ile Ile Asp Ser Leu Cys Lys Asp Gly Arg
811                               260                               265                               270
812 cat agc gat tct caa aat ctt ttc act gaa atg caa gag aaa gga atc 864
813 His Ser Asp Ser Gln Asn Leu Phe Thr Glu Met Gln Glu Lys Gly Ile
814                               275                               280                               285
815 ttt cca gat tta ttt acc tac aac tgt atg atc aac ggg ttt tgt agc 912
816 Phe Pro Asp Leu Phe Thr Tyr Asn Cys Met Ile Asn Gly Phe Cys Ser
817                               290                               295                               300
818 tct ggt aga tgg atc gac gcg gag cag ttg ttg caa gaa atg tta gaa 960
819 Ser Gly Arg Trp Ile Asp Ala Glu Gln Leu Leu Gln Glu Met Leu Glu
820 305                               310                               315                               320
821 agg aag atc agc cct gat gtt gta act tat aat gct ttg atc aat gca 1008
822 Arg Lys Ile Ser Pro Asp Val Val Thr Tyr Asn Ala Leu Ile Asn Ala
823                               325                               330                               335
824 ttt gtc aag gaa ggc aag ttc ttt gag gct gaa gaa tta tac gat gag 1056
825 Phe Val Lys Glu Gly Lys Phe Phe Glu Ala Glu Glu Leu Tyr Asp Glu
826                               340                               345                               350
827 atg ctt cct agg ggt ata atc cct aat aca atc aca tat agt tca atg 1104
828 Met Leu Pro Arg Gly Ile Ile Pro Asn Thr Ile Thr Tyr Ser Ser Met
829                               355                               360                               365
830 atc gat gga ttt tgc aaa cag aat cgt ctt gat gct gct gag cac atg 1152
831 Ile Asp Gly Phe Cys Lys Gln Asn Arg Leu Asp Ala Ala Glu His Met
832                               370                               375                               380
833 ttt tat ttg atg cct acc aag ggc tgc tct ccg gac gta ttc act ttc 1200
834 Phe Tyr Leu Met Pro Thr Lys Gly Cys Ser Pro Asp Val Phe Thr Phe
835 385                               390                               395                               400
836 aat act ctc ata gac gga tat cgt ggg gct aag agg ata gat gat gga 1248
837 Asn Thr Leu Ile Asp Gly Tyr Arg Gly Ala Lys Arg Ile Asp Asp Gly
838                               405                               410                               415
839 atg gaa ctt ctc cat gag atg act gaa gca gga tta gtt gct aac aca 1296
840 Met Glu Leu Leu His Glu Met Thr Glu Ala Gly Leu Val Ala Asn Thr
841                               420                               425                               430
842 gtt act tac aac act ctt att cac ggg ttt tgt cag gtg ggc gat ctt 1344
843 Val Thr Tyr Asn Thr Leu Ile His Gly Phe Cys Gln Val Gly Asp Leu
844                               435                               440                               445
845 act gct gct cta gac ctt cta cat gag atg att tct agt ggt gtg tgc 1392
846 Thr Ala Ala Leu Asp Leu Leu His Glu Met Ile Ser Ser Gly Val Cys
847                               450                               455                               460
848 cct aat gtc gtt act tgt agc act ttg ctg gat ggt ctc tgc gat aac 1440
849 Pro Asn Val Val Thr Cys Ser Thr Leu Leu Asp Gly Leu Cys Asp Asn
850 465                               470                               475                               480
851 ggg aaa cta aaa gat gca tgg gaa ctg ttt aag gtt atg cag aag agt 1488
852 Gly Lys Leu Lys Asp Ala Trp Glu Leu Phe Lys Val Met Gln Lys Ser
853                               485                               490                               495
854 aag atg gat ctt gat gct agt cac ccc ttc aat ggt gtg gaa cct gat 1536
855 Lys Met Asp Leu Asp Ala Ser His Pro Phe Asn Gly Val Glu Pro Asp
856                               500                               505                               510

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857 gtt caa act tac aat ata ttg atc agc ggc ttg atc aat gaa ggg aag 1584
858 Val Gln Thr Tyr Asn Ile Leu Ile Ser Gly Leu Ile Asn Glu Gly Lys
859          515          520          525
860 ttt tta gag gct gag gaa tta tac aag gag atg ccc cac agg ggt ata 1632
861 Phe Leu Glu Ala Glu Glu Leu Tyr Lys Glu Met Pro His Arg Gly Ile
862          530          535          540
863 gtc cca gat act att acc tat agc tca atg atc gat gga cta tgc aag 1680
864 Val Pro Asp Thr Ile Thr Tyr Ser Ser Met Ile Asp Gly Leu Cys Lys
865 545          550          555          560
866 cag agc cgc ctg gat gag gct aca caa atg ttt gat tcg atg ggt agc 1728
867 Gln Ser Arg Leu Asp Glu Ala Thr Gln Met Phe Asp Ser Met Gly Ser
868          565          570          575
869 aag agc ttc tct cca aac gta gtg acc ttt act aca ctc att gat ggc 1776
870 Lys Ser Phe Ser Pro Asn Val Val Thr Phe Thr Thr Leu Ile Asp Gly
871          580          585          590
872 tac tgt aaa gca gga agg gtt gat gat ggg ctg gag ctt ttc tgc gag 1824
873 Tyr Cys Lys Ala Gly Arg Val Asp Asp Gly Leu Glu Leu Phe Cys Glu
874          595          600          605
875 atg ggt aga aga ggg ata gtt gct aat aca att act tac atc act ttg 1872
876 Met Gly Arg Arg Gly Ile Val Ala Asn Thr Ile Thr Tyr Ile Thr Leu
877          610          615          620
878 att cgt ggt ttt cgc aat gtg ggt aat att aat ggg gct cta gac att 1920
879 Ile Arg Gly Phe Arg Asn Val Gly Asn Ile Asn Gly Ala Leu Asp Ile
880 625          630          635          640
881 ttc cag gag atg att tca agt ggt gtg tat cct ggt atc att act atc 1968
882 Phe Gln Glu Met Ile Ser Ser Gly Val Tyr Pro Gly Ile Ile Thr Ile
883          645          650          655
884 cgc agt atg ctg act ggt tta tgg agt aaa gag gaa cta aaa agg aca 2016
885 Arg Ser Met Leu Thr Gly Leu Trp Ser Lys Glu Glu Leu Lys Arg Thr
886          660          665          670
887 gtg gca atg ctt gag gaa ctg cag atg agt gtg ggg tat cag ttg gag 2064
888 Val Ala Met Leu Glu Glu Leu Gln Met Ser Val Gly Tyr Gln Leu Glu
889          675          680          685
890 gat gaa tga          2073

```

E-->

891 Asp Glu ~~Xaa~~ *Delete Xaa*

892 690

893 <210> SEQ ID NO: 19

894 <211> LENGTH: 691 *690*

895 <212> TYPE: PRI

896 <213> ORGANISM: Raphanus sativus

W-X

897 <400> SEQUENCE: 19

898 Met Leu Ala Arg Val Cys Gly Phe Lys Cys Ser Ser Ser Pro Ala Val

899 1 5 10 15

900 Ser Ala Ala Arg Leu Phe Cys Thr Arg Ser Ile Arg Asp Thr Leu Ala

901 20 25 30

902 Lys Ala Ser Arg Asp Gly Glu Ser Cys Glu Ala Gly Phe Gly Gly Glu

903 35 40 45

904 Ser Leu Lys Leu Gln Ser Gly Phe His Glu Ile Lys Gly Leu Glu Asp

905 50 55 60

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/613,053

DATE: 07/29/2003

TIME: 11:29:14

Input Set : A:\PTO.YF.txt

Output Set: N:\CRF4\07292003\J613053.raw

```

906 Ala Ile Asp Leu Phe Ser Asp Met Leu Arg Ser Arg Pro Leu Pro Ser
907 65 70 75 80
908 Val Val Asp Phe Cys Lys Leu Met Gly Val Val Val Arg Met Lys Arg
909 85 90 95
910 Pro Asp Val Val Ile Ser Leu His Lys Lys Met Glu Met Arg Arg Ile
911 100 105 110
912 Pro Cys Asp Ala Tyr Ser Phe Asn Ile Leu Ile Lys Cys Phe Cys Ser
913 115 120 125
914 Cys Ser Lys Leu Pro Phe Ala Leu Ser Thr Phe Gly Lys Leu Thr Lys
915 130 135 140
916 Leu Gly Leu His Pro Asp Val Val Thr Phe Thr Thr Leu Leu His Gly
917 145 150 155 160
918 Leu Cys Val Glu Asn Arg Gly Ser Glu Ala Leu Asn Leu Phe His Gln
919 165 170 175
920 Met Phe Glu Thr Thr Cys Arg Pro Asn Val Val Thr Phe Thr Thr Leu
921 180 185 190
922 Met Asn Gly Leu Cys Arg Glu Gly Arg Ile Val Glu Ala Val Ala Leu
923 195 200 205
924 Leu Asp Arg Met Met Glu Asp Gly Leu Gln Pro Thr Gln Ile Thr Tyr
925 210 215 220
926 Gly Thr Ile Val Asp Gly Met Cys Lys Lys Gly Asp Thr Val Ser Ala
927 225 230 235 240
928 Leu Asn Leu Leu Arg Lys Met Glu Glu Val Ser His Ile Ile Pro Asn
929 245 250 255
930 Val Val Ile Tyr Ser Ala Ile Ile Asp Ser Leu Cys Lys Asp Gly Arg
931 260 265 270
932 His Ser Asp Ser Gln Asn Leu Phe Thr Glu Met Gln Glu Lys Gly Ile
933 275 280 285
934 Phe Pro Asp Leu Phe Thr Tyr Asn Cys Met Ile Asn Gly Phe Cys Ser
935 290 295 300
936 Ser Gly Arg Trp Ile Asp Ala Glu Gln Leu Leu Gln Glu Met Leu Glu
937 305 310 315 320
938 Arg Lys Ile Ser Pro Asp Val Val Thr Tyr Asn Ala Leu Ile Asn Ala
939 325 330 335
940 Phe Val Lys Glu Gly Lys Phe Phe Glu Ala Glu Glu Leu Tyr Asp Glu
941 340 345 350
942 Met Leu Pro Arg Gly Ile Ile Pro Asn Thr Ile Thr Tyr Ser Ser Met
943 355 360 365
944 Ile Asp Gly Phe Cys Lys Gln Asn Arg Leu Asp Ala Ala Glu His Met
945 370 375 380
946 Phe Tyr Leu Met Pro Thr Lys Gly Cys Ser Pro Asp Val Phe Thr Phe
947 385 390 395 400
948 Asn Thr Leu Ile Asp Gly Tyr Arg Gly Ala Lys Arg Ile Asp Asp Gly
949 405 410 415
950 Met Glu Leu Leu His Glu Met Thr Glu Ala Gly Leu Val Ala Asn Thr
951 420 425 430
952 Val Thr Tyr Asn Thr Leu Ile His Gly Phe Cys Gln Val Gly Asp Leu
953 435 440 445
954 Thr Ala Ala Leu Asp Leu Leu His Glu Met Ile Ser Ser Gly Val Cys

```

RAW SEQUENCE LISTING

DATE: 07/29/2003

PATENT APPLICATION: US/10/613,053

TIME: 11:29:14

Input Set : A:\PTO.YF.txt

Output Set: N:\CRF4\07292003\J613053.raw

```

955      450      455      460
956 Pro Asn Val Val Thr Cys Ser Thr Leu Leu Asp Gly Leu Cys Asp Asn
957 465      470      475      480
958 Gly Lys Leu Lys Asp Ala Trp Glu Leu Phe Lys Val Met Gln Lys Ser
959      485      490      495
960 Lys Met Asp Leu Asp Ala Ser His Pro Phe Asn Gly Val Glu Pro Asp
961      500      505      510
962 Val Gln Thr Tyr Asn Ile Leu Ile Ser Gly Leu Ile Asn Glu Gly Lys
963      515      520      525
964 Phe Leu Glu Ala Glu Glu Leu Tyr Lys Glu Met Pro His Arg Gly Ile
965      530      535      540
966 Val Pro Asp Thr Ile Thr Tyr Ser Ser Met Ile Asp Gly Leu Cys Lys
967 545      550      555      560
968 Gln Ser Arg Leu Asp Glu Ala Thr Gln Met Phe Asp Ser Met Gly Ser
969      565      570      575
970 Lys Ser Phe Ser Pro Asn Val Val Thr Phe Thr Thr Leu Ile Asp Gly
971      580      585      590
972 Tyr Cys Lys Ala Gly Arg Val Asp Asp Gly Leu Glu Leu Phe Cys Glu
973      595      600      605
974 Met Gly Arg Arg Gly Ile Val Ala Asn Thr Ile Thr Tyr Ile Thr Leu
975      610      615      620
976 Ile Arg Gly Phe Arg Asn Val Gly Asn Ile Asn Gly Ala Leu Asp Ile
977 625      630      635      640
978 Phe Gln Glu Met Ile Ser Ser Gly Val Tyr Pro Gly Ile Ile Thr Ile
979      645      650      655
980 Arg Ser Met Leu Thr Gly Leu Trp Ser Lys Glu Glu Leu Lys Arg Thr
981      660      665      670
982 Val Ala Met Leu Glu Glu Leu Gln Met Ser Val Gly Tyr Gln Leu Glu
983      675      680      685
E--> 984 Asp Glu Xaa delete
985      690
1024 <210> SEQ ID NO: 21
1025 <211> LENGTH: 171
1026 <212> TYPE: DNA PRT ←
1027 <213> ORGANISM: Raphanus raphanistrum
w-OK 1028 <400> SEQUENCE: 21
1029 Met Glu Arg Pro Asp Leu Val Ile Ser Leu Tyr Gln Lys Met Glu Arg
1030 1 5 10 15
1031 Lys Gln Ile Pro Cys Asp Val Tyr Ser Phe Asn Ile Leu Ile Lys Cys
1032 20 25 30
1033 Phe Cys Ser Cys Ser Lys Leu Pro Phe Ala Leu Ser Thr Phe Gly Lys
1034 35 40 45
1035 Ile Thr Lys Leu Gly Leu His Pro Asp Val Ala Thr Phe Asn Thr Leu
1036 50 55 60
1037 Leu His Gly Leu Cys Leu Asp Lys Arg Val Ser Glu Ala Leu Asp Leu
1038 65 70 75 80
1039 Phe His Gln Met Phe Glu Thr Thr Cys Arg Pro Asn Ile Ile Thr Phe
1040 85 90 95
1041 Thr Thr Leu Met Asn Gly Leu Cys Tyr Glu Gly Arg Val Val Glu Ala

```

RAW SEQUENCE LISTING

DATE: 07/29/2003

PATENT APPLICATION: US/10/613,053

TIME: 11:29:14

Input Set : A:\PTO.YF.txt

Output Set: N:\CRF4\07292003\J613053.raw

1042 100 105 110
 1043 Val Ala Leu Leu Asp Arg Met Leu Glu Asp Gly Leu Gln Pro Asp Gln
 1044 115 120 125
 1045 Ile Thr Tyr Gly Thr Ile Val Asp Gly Met Cys Lys Met Gly Asp Thr
 1046 130 135 140
 1047 Val Ser Ala Leu Asn Leu Leu Arg Lys Met Glu Glu Leu Ser His Ile
 1048 145 150 155 160
 1049 Lys Pro Asn Val Val Ile Tyr Ser Ala Ile Ile
 1050 165 170
 1051 <210> SEQ ID NO: 22
 1052 <211> LENGTH: 2073
 1053 <212> TYPE: DNA
 1054 <213> ORGANISM: Raphanus
 1055 <400> SEQUENCE: 22
 1056 atgtttggcta gggtttgttg attcaagtgt tcttcttctc ctgctgwgctc tgcggctaga 60
 E--> 1057 **ttgttctgta cgagatcgat tctgtatact ctggccaagg caagcrgrga k**~~nnnnnnngt~~ 120
 1058 tgcgaagcag gttttggagg agagagtttg aagctgcaaa gtgggttttca tgaaatcaaa 180
 1059 ggttttagagg atgcgattga tttgttcagt gacatgcttc gatctcgctcc tttaccttct. 240
 1060 gtggttgatt tctgtaaatt gatgggtgtg gtggtgagra tgraacgccc ggatsttgtg 300
 1061 atttctctcy atmaraagat ggaaakgmrr crsattcsat gtgatrtyata cagcttyaat 360
 1062 attctgataa artgtttctg cagytgctct aagctbcccet ttgctttgtc tacatttggg 420
 1063 aagmtcacca agcttggact ccaccctgat gttgytacct tcamcaccct kctccaygga 480
 1064 ttrtgystkg awrakagggk ttctgaagcy ttgratttkt ttcatacaaat gtttgaaacg 540
 1065 rcatgtaggc csaayrtcrt aacsttyacc ackytagatg acggtctttg cyrcgagggt 600
 1066 agarttgtcg aagcygtagc tctrcttgat cggatgmtrg aagatggctc ccagcctrmc 660
 1067 cagattactt ayggaacaat ygtagayggg atgtgttaaga wgggagayac tgtgtctgca 720
 1068 ytgaatctkc tgaggaagat ggaggagktg agccacatca waccacatgt kgtaatctat 780
 1069 agtgcmatca ttgatagcct ttgtaaagac ggacgtcata gcgatkcwca aaatcttttc 840
 1070 actgaaatgc aagagaaaag aatctttccm gatttattta cctacaacwg tatgatmrwy 900
 1071 ggktttttga gctctggtag atggakcgac gcggagcagt tgttgcaaga aatgttagaa 960
 1072 aggaagatca gccctgatgt tgtaacttat aatgcittga tcaatgcatt tgtcaaggaa 1020
 1073 ggcaagttct ttgaggctga agaattatac gatgagatgc ttccwagggg tataatccct 1080
 1074 aatacaatca catatagtct aatgatcgat ggattttgca aacagaatcg tcttgatgct 1140
 1075 gctgagcaca tgttttattt gatgsctacc aagggctgct ctccsracst awtcactttc 1200
 1076 aatactctca tagacggata tygtggggct aagaggatag atgatggaat ggaacttctc 1260
 1077 catgagatga ctgaarcagg attagtgtgct racacarya cttacaacac tcttattcac 1320
 1078 gggtytrtc wgggtggcga tcttamtgct gctctagacc ttytacawga gatgatyct 1380
 1079 agtggktgt gccctratrt cgttacttgt rrcactttgc tggatggctc ctgcgataay 1440
 1080 gggaaactaa aagatgcatk ggaamtgttt aaggttatgc agaagagtaa gawggatctt 1500
 1081 gatgctagtc accccttcaa tgggtgtgaa cctgatgttc aaacttacia tatattgac 1560
 1082 agcggcttga tcaatgaagg gaagttttta gaggygagg aattatacra ggagatgccc 1620
 1083 cacaggggta tagtcccaga tactatyacc tatagctcaa tgatcgatgg aytatgcaag 1680
 1084 cagagccgcc trgatgaggc tacacaaatg tttgattcga tgggtagcaa gagcttctct 1740
 1085 ccaaacgtag tgacctttac tacactcatt ratggctact gtaargcagg aaggggttgat 1800
 1086 gatgggctgg agcttttctg cgagatgggt mgaagaggga tagttgctaa yrcaattact 1860
 1087 tacatcactt tgattygtgg ttttcgyaaw gtgggtaata ttaatggggc tctagacatt 1920
 1088 ttccaggaga tgatttcaag tgggtgtgat cctgrtayca ttacyatccg cartatgctg 1980
 1089 actggtttat ggagtaaaga ggaactaaaa aggrcagtg caatgcttga graactgcag 2040
 1090 atgagtrtgg rkywwymrtt kgrggrwkra tga 2073

see
 P. 13
 for
 error
 explanation

RAW SEQUENCE LISTING

DATE: 07/29/2003

PATENT APPLICATION: US/10/613,053

TIME: 11:29:14

Input Set : A:\PTO.YF.txt

Output Set: N:\CRF4\07292003\J613053.raw

1091 <210> SEQ ID NO: 23

1092 <211> LENGTH: 2073

1093 <212> TYPE: DNA

1094 <213> ORGANISM: Raphanus

OK> 1095 <400> SEQUENCE: 23

E--> 1097 ~~ttgtttctgta~~ ~~cgagatcgat~~ ~~tcgtgatact~~ ~~ctggccaagg~~ ~~caagcrgrga~~ ~~ktnnnnnnngt~~ 120

1096 atgtttggcta gggtttgtgg attcaagtgt tcttcttctc ctgctgwgtc tgcgactaga 60

1098 tgcgaagcag gttttggagg agagagtttg aagctgcaaa gtgggtttca tgaaatcaaa 180

1099 ggttttagagg atgcgattga tttgttcagt gacatgcttc gatctcgtcc tttaccttct 240

1100 gtggttgatt tctgtaaatt gatgggtgtg gtggtgagra tgraacgccc ggatsttgtg 300

1101 atttctctcy atmagaagat ggaaakgmrr crsattcsat gtgatriyata cagcttcaat 360

1102 attctgataa artgtttctg cagctgctct aagctscctt ttgctttgtc tacatttggg 420

1103 aagmtcacca agcttggact ccaccctgat gttgttacct tcaccaccct kctccaygga 480

1104 ttrtgygtgg aaratagggk ttctgaagcy ttgratttkt ttcatacaaat gtttgaaacg 540

1105 rcatgtaggc ccaatgtcgt aaccttcacc actttgatga acggtctttg ccgcgagggt 600

1106 agaattgtcg aagccgtagc tctrcttgat cggatgatgg aagatggtct ccagcctacc 660

1107 cagattactt atggaacaat cgtagatggg atgtgtaaga agggagatac tgtgtctgca 720

1108 ctgaatctgc tgaggaagat ggaggagggt agccacatca taccacatgt tgtaatctat 780

1109 agtgcaatca ttgatagcct ttgtaaagac ggacgtcata gcgatkcwca aaatcttttc 840

1110 actgaaatgc aagagaaaagg aatctttccm gatttattta cctacaacwg tatgatmrwy 900

1111 ggktttttga gctctggtag atggakcgac gcggagcagt tgttgcaaga aatgttagaa 960

1112 aggaagatca gccctgatgt tgtaacttat aatgctttga tcaatgcatt tgtcaaggaa 1020

1113 ggcaagttct ttgaggctga agaattatac gatgagatgc ttccwagggg tataatccct 1080

1114 aatacaatca catatagttc aatgatcgat ggattttgca aacagaatcg tcttgatgct 1140

1115 gctgagcaca tgttttatth gatgsctacc aagggtgctc ctccsracst awtcaacttc 1200

1116 aatactctca tagacggata tygtggggct aagaggatag atgatggaat ggaacttctc 1260

1117 catgagatga ctgaarcagg attagttgct racacaryta cttacaacac tcttattcac 1320

1118 gggttytrtc wgggtggcgga tcttamtgct gctctagacc ttytacawga gatgatytct 1380

1119 agtggtktgt gccctratrt cgttacttgt rrcactttgc tggatggtct ctgcgataay 1440

1120 gggaaactaa aagatgcatk ggaamtgttt aagggtatgc agaagagtaa gawggatctt 1500

1121 gatgctagtc accccttcaa tgggtgtggaa cctgatgttc aaacttacia tatattgatc 1560

1122 agcggcttga tcaatgaagg gaagttttta gaggygagg aattatacra ggagatgccc 1620

1123 cacaggggta tagtcccaga tactatyacc tatagctcaa tgatcgatgg aytatgcaag 1680

1124 cagagccgcc trgatgaggc tacacaaatg tttgattcga tgggtagcaa gagcttctct 1740

1125 ccaaacgtag tgacctttac tacactcatt ratggctact gtaargcagg aagggttgat 1800

1126 gatgggctgg agcttttctg cgagatgggt mgaagaggga tagttgctaa yrcaattact 1860

1127 tacatcactt tgattygtgg ttttcgyaaw gtgggtaata ttaatggggc tctagacatt 1920

1128 ttccaggaga tgatttcaag tggtgtgtat cctgrtayca ttacyatccg cartatgctg 1980

1129 actggtttat ggagtaaaga ggaactaaaa aggrcagtgg caatgcttga graactgcag 2040

1130 atgagtrtgg rkywwymrtt kgrggrwkra tga 2073

sep.13

see pp 14-15 for more error

VARIABLE LOCATION SUMMARY

DATE: 07/29/2003

PATENT APPLICATION: US/10/613,053

TIME: 11:29:16

Input Set : A:\PTO.YF.txt

Output Set: N:\CRF4\07292003\J613053.raw

Use of n's or Xaa's (NEW RULES):

Use of n's and/or Xaa's have been detected in the Sequence Listing.

Use of <220> to <223> is MANDATORY if n's or Xaa's are present.

in <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

error explanation

Seq#:16; Xaa Pos. 688

Seq#:17; Xaa Pos. 688

Seq#:18; Xaa Pos. 691

Seq#:19; Xaa Pos. 691

Seq#:22; N Pos. 113,114,115,116,117,118

Seq#:23; N Pos. 113,114,115,116,117,118

Seq#:26; Xaa Pos. 16,36,37,95,99,104,105,109,110,111,113,116,142,152,155

Seq#:26; Xaa Pos. 163,164,165,167,172,173,186,187,198,202,213,220,234,250

Seq#:26; Xaa Pos. 254,276,297,300,309,389,396,397,398,408,426,431,433,443

Seq#:26; Xaa Pos. 444,449,456,463,466,467,471,487,489,498,537,591,618,626

Seq#:26; Xaa Pos. 630,652,653,658,672,678,683,684,685,686,687,688,689,690

Seq#:27; Xaa Pos. 16,36,37,95,99,104,105,109,110,111,113,116,142,165,167

Seq#:27; Xaa Pos. 172,173,276,297,300,309,389,396,397,398,408,426,431,433

Seq#:27; Xaa Pos. 443,444,449,456,463,466,467,471,487,489,498,537,591,618

Seq#:27; Xaa Pos. 626,630,652,653,658,672,678,683,684,685,686,687,688,689

Seq#:27; Xaa Pos. 690

Seq#:28; Xaa Pos. 111,114,140,150,153,161,162,163,170,171,184,185,196,200

Seq#:28; Xaa Pos. 211,218,232,248,252

Seq#:29; Xaa Pos. 140,170,171

10/6/3, 053 14

<210> 26
<211> 690
<212> PRT
<213> Raphanus
<220>

<221> Xaa
<222> 16
<223> Glu or Val
<221> Xaa
<222> 36
<223> Arg or none

<221> Xaa
<223> 37 Asp or none

→ <2227> move this to <2227> line. it
belongs on
<2227> line

Please correct any similar
errors,
throughout.
Sequence Listing

10/6/3,053

15

<210> 41 ← last sequence in submitted file
<211> 21
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Synthetic DNA
<400> 41
gacatgtagg cccaatgtcg t 21

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/613,053

DATE: 07/29/2003

TIME: 11:29:16

Input Set : A:\PTO.YF.txt

Output Set: N:\CRF4\07292003\J613053.raw

L:3 M:283 W: Missing Blank Line separator, <120> field identifier
 L:5 M:283 W: Missing Blank Line separator, <130> field identifier
 L:6 M:270 C: Current Application Number differs, Replaced Current Application No
 L:6 M:271 C: Current Filing Date differs, Replaced Current Filing Date
 L:6 M:283 W: Missing Blank Line separator, <160> field identifier
 L:7 M:283 W: Missing Blank Line separator, <210> field identifier
 L:11 M:283 W: Missing Blank Line separator, <400> field identifier
 L:159 M:283 W: Missing Blank Line separator, <400> field identifier
 L:293 M:283 W: Missing Blank Line separator, <400> field identifier
 L:384 M:283 W: Missing Blank Line separator, <220> field identifier
 L:386 M:283 W: Missing Blank Line separator, <400> field identifier
 L:392 M:283 W: Missing Blank Line separator, <220> field identifier
 L:394 M:283 W: Missing Blank Line separator, <400> field identifier
 L:400 M:283 W: Missing Blank Line separator, <220> field identifier
 L:402 M:283 W: Missing Blank Line separator, <400> field identifier
 L:408 M:283 W: Missing Blank Line separator, <220> field identifier
 L:410 M:283 W: Missing Blank Line separator, <400> field identifier
 L:416 M:283 W: Missing Blank Line separator, <220> field identifier
 L:418 M:283 W: Missing Blank Line separator, <400> field identifier
 L:424 M:283 W: Missing Blank Line separator, <220> field identifier
 L:426 M:283 W: Missing Blank Line separator, <400> field identifier
 L:432 M:283 W: Missing Blank Line separator, <220> field identifier
 L:434 M:283 W: Missing Blank Line separator, <400> field identifier
 L:440 M:283 W: Missing Blank Line separator, <220> field identifier
 L:442 M:283 W: Missing Blank Line separator, <400> field identifier
 L:448 M:283 W: Missing Blank Line separator, <220> field identifier
 L:450 M:283 W: Missing Blank Line separator, <400> field identifier
 L:456 M:283 W: Missing Blank Line separator, <220> field identifier
 L:458 M:283 W: Missing Blank Line separator, <400> field identifier
 L:465 M:283 W: Missing Blank Line separator, <220> field identifier
 L:467 M:283 W: Missing Blank Line separator, <400> field identifier
 L:474 M:283 W: Missing Blank Line separator, <400> field identifier
 L:535 M:283 W: Missing Blank Line separator, <400> field identifier
 L:663 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:16 ✓
 L:669 M:283 W: Missing Blank Line separator, <400> field identifier
 L:754 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:17 ✓
 L:760 M:283 W: Missing Blank Line separator, <400> field identifier
 L:891 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:18 ✓
 L:897 M:283 W: Missing Blank Line separator, <400> field identifier
 L:984 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:19 ✓
 L:990 M:283 W: Missing Blank Line separator, <400> field identifier
 L:1028 M:283 W: Missing Blank Line separator, <400> field identifier ✓
 L:1050 M:301 E: (44) No Sequence Data was Shown, SEQ ID:21 ✓
 L:1050 M:252 E: No. of Seq. differs, <211> LENGTH:Input:171 Found:0 SEQ:21 ✓
 L:1055 M:283 W: Missing Blank Line separator, <400> field identifier
 L:1057 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:22 ✓
 L:1095 M:283 W: Missing Blank Line separator, <400> field identifier
 L:1097 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:23 ✓

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/613,053

DATE: 07/29/2003

TIME: 11:29:16

Input Set : A:\PTO.YF.txt

Output Set: N:\CRF4\07292003\J613053.raw

L:1135 M:283 W: Missing Blank Line separator, <400> field identifier
L:1175 M:283 W: Missing Blank Line separator, <400> field identifier
L:1215 M:283 W: Missing Blank Line separator, <220> field identifier
L:1216 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
L:1219 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
L:1222 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:26
L:1222 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
L:1224 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:26
L:1224 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
L:1227 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:26
L:1227 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
L:1230 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:26
L:1230 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
L:1233 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:26
L:1233 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
L:1236 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:26
L:1236 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
L:1239 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:26
L:1239 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
L:1242 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:26
L:1242 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
L:1245 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:26
L:1245 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
L:1248 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:26
L:1248 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
L:1251 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:26
L:1251 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
L:1254 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:26
L:1254 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
L:1257 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:26
L:1257 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
L:1260 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:26
L:1260 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
L:1263 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:26
L:1263 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
L:1266 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:26
L:1266 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
L:1269 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:26
L:1269 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
L:1272 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:26
L:1272 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
L:1275 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:26
L:1275 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
L:1278 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:26
L:1278 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
L:1281 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:26
L:1281 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
L:1284 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:26
L:1284 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/613,053

DATE: 07/29/2003

TIME: 11:29:16

Input Set : A:\PTO.YF.txt

Output Set: N:\CRF4\07292003\J613053.raw

L:1287 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:26
L:1287 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
L:1290 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:26
L:1290 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
L:1293 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:26
L:1293 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
L:1296 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:26
L:1296 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
L:1299 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:26
L:1299 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
L:1302 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:26
L:1302 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
L:1305 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:26
L:1305 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
L:1308 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:26
L:1308 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
L:1311 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:26
L:1311 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
L:1314 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:26
L:1314 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
L:1317 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:26
L:1317 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
L:1320 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:26
L:1320 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
L:1323 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:26
L:1323 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
L:1326 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:26
L:1326 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
L:1329 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:26
L:1329 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
L:1332 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:26
L:1332 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
L:1335 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:26
L:1335 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
L:1338 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:26
L:1338 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
L:1341 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:26
L:1341 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
L:1344 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:26
L:1344 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
L:1347 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:26
L:1347 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
L:1350 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:26
L:1350 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
L:1353 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:26
L:1353 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
L:1356 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:26
L:1356 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
L:1359 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:26

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/613,053

DATE: 07/29/2003

TIME: 11:29:16

Input Set : A:\PTO.YF.txt

Output Set: N:\CRF4\07292003\J613053.raw

L:1359 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
L:1362 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:26
L:1362 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
L:1365 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:26
L:1368 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:26
L:1428 M:283 W: Missing Blank Line separator, <400> field identifier
L:1429 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26 after pos.:0
M:341 Repeated in SeqNo=26
L:1521 M:283 W: Missing Blank Line separator, <220> field identifier
L:1695 M:283 W: Missing Blank Line separator, <400> field identifier
L:1696 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27 after pos.:0
M:341 Repeated in SeqNo=27
L:1788 M:283 W: Missing Blank Line separator, <220> field identifier
L:1795 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:1798 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:1801 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:1804 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:1807 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:1810 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:1813 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:1816 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:1819 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:1822 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:1825 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:1828 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:1831 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:1834 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:1837 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:1840 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:1843 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:1846 M:283 W: Missing Blank Line separator, <400> field identifier
L:1859 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28 after pos.:96
M:341 Repeated in SeqNo=28
L:1937 M:283 W: Missing Blank Line separator, <220> field identifier
L:1947 M:283 W: Missing Blank Line separator, <400> field identifier
L:1964 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29 after pos.:128
M:341 Repeated in SeqNo=29
L:2038 M:283 W: Missing Blank Line separator, <220> field identifier
L:2040 M:283 W: Missing Blank Line separator, <400> field identifier
L:6 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (39) Counted (41)